

APPENDIX A
CLEAN VERSION OF SUBSTITUTE SEQUENCE LISTING
(Application Serial No. 10/046,671)



SEQUENCE LISTING

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Huurne ter, Anna A.H.M
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<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671
<141> 2002-01-14

<150> PCT/NL00/00493
<151> 2000-07-13

<150> EP 99202316.8
<151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

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<220>
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ggggacccgc gaacgg 16

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<221> misc_feature
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 <210> 21
 <211> 17
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 <223> Primer HY2M

 <400> 21
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 <223> Primer T7EcoRI

 <400> 22
 ggaattctaa tacgactcac tatagg 26

 <210> 23
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer HY3M

 <400> 23
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 <220>
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 <223> Primer M13F

<400> 24
gtaaaacgac ggccagt 17

<210> 25
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<220>
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<210> 26
<211> 17
<212> DNA
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<220>
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<223> Primer ANC2

<400> 26
ctgcctgtcc tggagcc 17

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<223> Primer HY4P

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<223> Primer ANC3

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cgatgggcgt tcgggtc 17

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<220>
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<223> Primer ANC5

<400> 29
cccatctgga gcatatcc

18

<210> 30
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<220>
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<400> 30
ttcacctggg gtactccg

18

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<223> Anchor

<400> 31
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<210> 32
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<223> Anchor primer

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gaaggatcca gaatcgatag

20

<210> 33
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 <400> 33
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 <220>
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 <222> (1)..(16)
 <223> Primer ANC1

 <400> 34
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 <211> 47
 <212> DNA
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 <220>
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 <222> (1)..(47)
 <223> Primer T7AC0

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 <211> 15
 <212> DNA
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 <222> (1)..(15)
 <223> Primer BNC1

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ggggggccccc gcagg 15

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<223> 5'-Terminus of the A-segment coding strand
of IBDV

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ugauacgauc 10

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<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the A-segment coding strand
of IBDV

<400> 39
agauacgauc 10

<210> 40
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>

<221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 40
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<210> 41
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> Consensus sequence corresponding to the
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 IBDV

<400> 41
 ggauacgauc 10

<210> 42
 <211> 4
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(4)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 42
 cggg 4

<210> 43
 <211> 8
 <212> RNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
 of the A-segment non-coding strand of IBDV

<400> 43
 cggguccc 8

<210> 44
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 44
cgggucccu

9

<210> 45
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 45
cgggucccc

9

<210> 46
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 46
cggguccccc c

11

<210> 47
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 47
cggguccccc cu 12

<210> 48
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 48
cggguccccc cc 12

<210> 49
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Consensus complementary sequence of the
5'-terminus of the A-segment non-coding strand of
IBDV

<400> 49
cggguccccc 9

<210> 50
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
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<222> (1)..(10)
<223> 5'-Terminus of the B-segment coding strand
of IBDV

<400> 50
ugauacgaug 10

<210> 51
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the B-segment coding strand
 of IBDV

<400> 51
 ggauacgaug 10

<210> 52
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<213> Infectious bursal disease virus

<220>
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 ggauacgaug 10

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<220>
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 <222> (1)..(8)
 <223> Complementary sequence of the 5'-terminus
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<400> 53
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<210> 54
 <211> 8
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<220>
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 <222> (1)..(8)
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<220>
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<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

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8

<210> 56
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<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 56
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9

<210> 57
<211> 10
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<220>
<221> misc_RNA
<222> (1)..(10)
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<210> 58
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<220>
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<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 58

ggggggccccc c

11

<210> 59

<211> 11

<212> RNA

<213> Infectious bursal disease virus

<220>

<221> misc_RNA

<222> (1)..(11)

<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

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11

<210> 60

<211> 10

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_RNA

<222> (1)..(10)

<223> Consensus complementary sequence of the
5'-terminus of the B-segment non-coding strand of
IBDV

<400> 60

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10

<210> 61

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolates D6948, rD6948, UK661
5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,
TKSM and HK46

<400> 61

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser

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                20                25                30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
      35                40                45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
      50                55                60
Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
      65                70                75                80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85                90                95
Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
      100                105                110
Gly Asp Gln Met Ser Trp Ser
      115

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<210> 62
<211> 119
<212> PRT
<213> Infectious bursal disease virus

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<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
      region of VP2 of IBDV isolate 96-B4

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<400> 62
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20                25                30
Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
      35                40                45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
      50                55                60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65                70                75                80
Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
      85                90                95
Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
      100                105                110
Gly Asp Gln Met Ser Trp Ser

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<210> 63
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 96-C4

<400> 63
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Leu Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu
 35 40 45
 Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 64
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of a IBDV isolate 96-C5

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 1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 65
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 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 97-B3

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 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 66
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>

<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate Zoontjes

<400> 66
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20 25 30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60
Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile
85 90 95
Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110
Gly Asp Gln Met Ser Trp Ser
115

<210> 67
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
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<400> 67

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      20          25          30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu
      35          40          45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
      50          55          60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65          70          75          80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85          90          95
Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala
      100          105          110
Gly Asp Gln Met Ser Trp Ser
      115

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<210> 68
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
      20          25          30
Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu
      35          40          45
Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr
      50          55          60
Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
      65          70          75          80
Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
      85          90          95

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Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

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<213> Infectious bursal disease virus

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<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate HK46-NT

<400> 69
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Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 70
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<222> (1)..(3260)
<223> Consensus cDNA sequence of IBDV A-segment

<400> 70

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<210> 71

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

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<210> 72

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBV A-segment

<400> 72

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<210> 73

<211> 964

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(964)

<223> cDNA sequence TY89-A of IBDV A-segment

<400> 73

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<210> 74
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> Consensus cDNA sequence of IBV B-segment

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gaggcggttg gggttgtagg tggttggaac taccactcc tgaacaaagc ytgcaagaay 2040
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gtcaacagac cagtcaacac yggkggrctm aaggcagtc gcaaygccct caagaccggy 2280
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<210> 75

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence CEF94-B of IBV B-segment

<400> 75

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tggatgcgac	agatagaagg	ggctgtttta	aaaccactc	tatctctccc	tattggagat	420
caggagtact	tcccaaagta	ctacccaaca	catcgcccta	gcaaggagaa	gccaatgcg	480
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2827

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<210> 76

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc_feature

<222> (1)..(2827)

<223> cDNA sequence D6948-B of IBV B-segment

<400> 76

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<210> 77
<211> 1012
<212> PRT
<213> Infectious bursal disease virus

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<222> (1)..(1012)
<223> Consensus sequence of IBDV polyprotein

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<223> The 'Xaa' at position 715 may be any amino acid

<400> 77

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 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
 85 90 95
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110
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 115 120 125
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
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 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Xaa Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
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 Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
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Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val 340 345 350		
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val 355 360 365		
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val 370 375 380		
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu 385 390 395 400		
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr 405 410 415		
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu 420 425 430		
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile 435 440 445		
Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro 450 455 460		
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu 465 470 475 480		
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser 485 490 495		
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala 500 505 510		
Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln 515 520 525		
Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly 530 535 540		
Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro 545 550 555 560		
Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn 565 570 575		
Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro 580 585 590		

Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
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 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
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 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
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 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe
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 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
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 785 790 795 800
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 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
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 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880

Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
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<210> 78
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein CEF94-PP

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 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr

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 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670

Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn

965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

 <210> 79
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein D6948-PP

 <400> 79
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
 85 90 95
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
 115 120 125
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
 225 230 235 240
 Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn
 275 280 285
 Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro
 290 295 300
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
 305 310 315 320
 Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr
 325 330 335
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460

Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Ile Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Tyr Gly Glu Ile Glu Asn Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Ser Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr Asp Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala

755					760					765					
Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser
770					775					780					
Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp
785					790					795					800
Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn
				805					810					815	
Phe	Leu	Ala	Asn	Ala	Pro	Gln	Ala	Gly	Ser	Lys	Ser	Gln	Arg	Ala	Lys
			820					825					830		
Tyr	Gly	Thr	Ala	Gly	Tyr	Gly	Val	Glu	Ala	Arg	Gly	Pro	Thr	Pro	Glu
		835					840					845			
Glu	Ala	Gln	Arg	Glu	Lys	Asp	Thr	Arg	Ile	Ser	Lys	Lys	Met	Glu	Thr
	850					855					860				
Met	Gly	Ile	Tyr	Phe	Ala	Thr	Pro	Glu	Trp	Val	Ala	Leu	Asn	Gly	His
865					870					875					880
Arg	Gly	Pro	Ser	Pro	Gly	Gln	Leu	Lys	Tyr	Trp	Gln	Asn	Thr	Arg	Glu
				885					890					895	
Ile	Pro	Asp	Pro	Asn	Glu	Asp	Tyr	Leu	Asp	Tyr	Val	His	Ala	Glu	Lys
			900					905					910		
Ser	Arg	Leu	Ala	Ser	Glu	Glu	Gln	Ile	Leu	Arg	Ala	Ala	Thr	Ser	Ile
		915					920					925			
Tyr	Gly	Ala	Pro	Gly	Gln	Ala	Glu	Pro	Pro	Gln	Ala	Phe	Ile	Asp	Glu
	930					935					940				
Val	Ala	Lys	Val	Tyr	Glu	Ile	Asn	His	Gly	Arg	Gly	Pro	Asn	Gln	Glu
945					950					955					960
Gln	Met	Lys	Asp	Leu	Leu	Leu	Thr	Ala	Met	Glu	Met	Lys	His	Arg	Asn
				965					970					975	
Pro	Arg	Arg	Ala	Pro	Pro	Lys	Pro	Lys	Pro	Lys	Pro	Asn	Ala	Pro	Thr
			980				985						990		
Gln	Arg	Pro	Pro	Gly	Arg	Leu	Gly	Arg	Trp	Ile	Arg	Ala	Val	Ser	Asp
		995				1000					1005				
Glu	Asp	Leu	Glu												
	1010														

<210> 80

<211> 290

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(290)

<223> Sequence of IBDV polyprotein TY89-PP

<400> 80

Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn
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Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu
20 25 30

Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg
35 40 45

Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu
50 55 60

Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala
65 70 75 80

Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu
85 90 95

Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly
100 105 110

Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala
115 120 125

Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly
130 135 140

Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly
145 150 155 160

Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro
165 170 175

Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg
180 185 190

Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly
195 200 205

Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala
210 215 220

Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met
225 230 235 240

Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg
245 250 255

Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg
260 265 270

Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp
275 280 285

Leu Glu
290

<210> 81
<211> 881
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(881)
<223> Consensus sequence of IBDV VP1

<220>
<221> MISC_FEATURE
<222> (4)
<223> The 'Xaa' at position 4 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (13)
<223> The 'Xaa' at position 13 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (61)
<223> The 'Xaa' at position 61 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (145). . . (147)
<223> The 'Xaa' at positions 145-147 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (287)
<223> The 'Xaa' at position 287 may be any amino acid

<220>
<221> MISC_FEATURE
<222> (390)
<223> The 'Xaa' at position 390 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (393)
 <223> The 'Xaa' at position 393 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (508)
 <223> The 'Xaa' at position 508 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (511)
 <223> The 'Xaa' at position 511 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (546)
 <223> The 'Xaa' at position 546 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (562)
 <223> The 'Xaa' at position 562 may be any amino acid

<220>
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 <222> (646)
 <223> The 'Xaa' at position 646 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (687)
 <223> The 'Xaa' at position 687 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (695)
 <223> The 'Xaa' at position 695 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (880) . . . (881)
 <223> The 'Xaa' at positions 880-881 may be any amino acid

<400> 81
 Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala
 1 5 10 15
 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser

35					40					45						
Arg	Leu	Ala	Lys	Phe	Leu	Arg	Glu	Asn	Gly	Tyr	Lys	Xaa	Leu	Gln	Pro	
50					55					60						
Arg	Ser	Leu	Pro	Glu	Asn	Glu	Glu	Tyr	Glu	Thr	Asp	Gln	Ile	Leu	Pro	
65					70					75					80	
Asp	Leu	Ala	Trp	Met	Arg	Gln	Ile	Glu	Gly	Ala	Val	Leu	Lys	Pro	Thr	
85					90					95						
Leu	Ser	Leu	Pro	Ile	Gly	Asp	Gln	Glu	Tyr	Phe	Pro	Lys	Tyr	Tyr	Pro	
100					105					110						
Thr	His	Arg	Pro	Ser	Lys	Glu	Lys	Pro	Asn	Ala	Tyr	Pro	Pro	Asp	Ile	
115					120					125						
Ala	Leu	Leu	Lys	Gln	Met	Ile	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Glu	Ala	
130					135					140						
Xaa	Xaa	Xaa	Leu	Lys	Asp	Glu	Val	Thr	Leu	Leu	Thr	Gln	Asn	Ile	Arg	
145					150					155					160	
Asp	Lys	Ala	Tyr	Gly	Ser	Gly	Thr	Tyr	Met	Gly	Gln	Ala	Thr	Arg	Leu	
165					170					175						
Val	Ala	Met	Lys	Glu	Val	Ala	Thr	Gly	Arg	Asn	Pro	Asn	Lys	Asp	Pro	
180					185					190						
Leu	Lys	Leu	Gly	Tyr	Thr	Phe	Glu	Ser	Ile	Ala	Gln	Leu	Leu	Asp	Ile	
195					200					205						
Thr	Leu	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Asp	Lys	Pro	Trp	Val	Pro	
210					215					220						
Leu	Thr	Arg	Val	Pro	Ser	Arg	Met	Leu	Val	Leu	Thr	Gly	Asp	Val	Asp	
225					230					235					240	
Gly	Xaa	Phe	Glu	Val	Glu	Asp	Tyr	Leu	Pro	Lys	Ile	Asn	Leu	Lys	Ser	
245					250					255						
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly	
260					265					270						
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Xaa	Leu	
275					280					285						
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu	
290					295					300						
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro	
305					310					315					320	
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn	
325					330					335						

Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380
 Ile Val Glu Trp Ile Xaa Ala Pro Xaa Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
 485 490 495
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Xaa Gln Pro Xaa Pro
 500 505 510
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540
 Val Xaa Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560
 Gln Xaa Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa
 865 870 875 880
 Xaa

<210> 82
 <211> 881
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(881)

<223> Sequence of IBDV CEF94-VP1

<400> 82

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Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
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Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
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Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
      35           40           45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
      50           55           60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
      65           70           75           80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
      85           90           95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
      100          105          110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
      115          120          125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
      130          135          140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
      145          150          155          160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
      165          170          175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
      180          185          190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
      195          200          205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
      210          215          220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
      225          230          235          240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
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245																250																255																		
Ser	Ser	Gly	Leu	Pro	Tyr	Val	Gly	Arg	Thr	Lys	Gly	Glu	Thr	Ile	Gly																																			
			260																	265																	270													
Glu	Met	Ile	Ala	Ile	Ser	Asn	Gln	Phe	Leu	Arg	Glu	Leu	Ser	Thr	Leu																																			
			275																	280																	285													
Leu	Lys	Gln	Gly	Ala	Gly	Thr	Lys	Gly	Ser	Asn	Lys	Lys	Lys	Leu	Leu																																			
			290																	295																	300													
Ser	Met	Leu	Ser	Asp	Tyr	Trp	Tyr	Leu	Ser	Cys	Gly	Leu	Leu	Phe	Pro																																			
			305																	310																	315													
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn																																			
			325																	330																	335													
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr																																			
			340																	345																	350													
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly																																			
			355																	360																	365													
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg																																			
			370																	375																	380													
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr																																			
			385																	390																	395													
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp																																			
			405																	410																	415													
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala																																			
			420																	425																	430													
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met																																			
			435																	440																	445													
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu																																			
			450																	455																	460													
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr																																			
			465																	470																	475													
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu																																			
			485																	490																	495													
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro																																			
			500																	505																	510													
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe																																			
			515																	520																	525													
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu																																			
			530																	535																	540													

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
545 550 555 560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
565 570 575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
580 585 590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
595 600 605

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
610 615 620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
625 630 635 640

Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
645 650 655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
660 665 670

Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
675 680 685

Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
690 695 700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
705 710 715 720

Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
725 730 735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
740 745 750

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
755 760 765

Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
770 775 780

Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
785 790 795 800

Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
805 810 815

Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
820 825 830

Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
835 840 845

Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
850 855 860

Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln
865 870 875 880

Pro

<210> 83

<211> 879

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(879)

<223> Sequence of IBV D6948-VP1

<400> 83

Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
100 105 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
115 120 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
130 135 140

Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
145 150 155 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu

	165		170		175
Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro	180		185		190
Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile	195		200		205
Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro	210		215		220
Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp	225		230		235
Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser	245		250		255
Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly	260		265		270
Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu	275		280		285
Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu	290		295		300
Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro	305		310		315
Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn	325		330		335
Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr	340		345		350
Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly	355		360		365
Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg	370		375		380
Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr	385		390		395
Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp	405		410		415
Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala	420		425		430
Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met	435		440		445
Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu	450		455		460

Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr	465	470	475	480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu	485	490	495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Lys	Gln	Pro	Ser	Pro	500	505	510	
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe	515	520	525	
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu	530	535	540	
Val	Pro	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu	545	550	555	560
Gln	Pro	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr	565	570	575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg	580	585	590	
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu	595	600	605	
Lys	Ser	Lys	Val	Gly	Ile	Glu	Gln	Ala	Tyr	Lys	Val	Val	Arg	Tyr	Glu	610	615	620	
Ala	Leu	Arg	Leu	Val	Gly	Gly	Trp	Asn	Tyr	Pro	Leu	Leu	Asn	Lys	Ala	625	630	635	640
Cys	Lys	Asn	Asn	Ala	Ser	Ala	Ala	Arg	Arg	His	Leu	Glu	Ala	Lys	Gly	645	650	655	
Phe	Pro	Leu	Asp	Glu	Phe	Leu	Ala	Glu	Trp	Ser	Glu	Leu	Ser	Glu	Phe	660	665	670	
Gly	Glu	Ala	Phe	Glu	Gly	Phe	Asn	Ile	Lys	Leu	Thr	Val	Thr	Pro	Glu	675	680	685	
Ser	Leu	Ala	Glu	Leu	Asn	Arg	Pro	Val	Pro	Pro	Lys	Pro	Pro	Asn	Val	690	695	700	
Asn	Arg	Pro	Val	Asn	Thr	Gly	Gly	Leu	Lys	Ala	Val	Ser	Asn	Ala	Leu	705	710	715	720
Lys	Thr	Gly	Arg	Tyr	Arg	Asn	Glu	Ala	Gly	Leu	Ser	Gly	Leu	Val	Leu	725	730	735	
Leu	Ala	Thr	Ala	Arg	Ser	Arg	Leu	Gln	Asp	Ala	Val	Lys	Ala	Lys	Ala	740	745	750	

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 84
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Consensus sequence of IBV VP5

<220>
 <221> MISC_FEATURE
 <222> (14)
 <223> The 'Xaa' at position 14 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (45)
 <223> The 'Xaa' at position 45 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (74)
 <223> The 'Xaa' at position 74 may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (125)
 <223> The 'Xaa' at position 125 may be any amino acid

<220>

<221> MISC_FEATURE

<222> (133)

<223> The 'Xaa' at position 133 may be any amino acid

<400> 84

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His
35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly
65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg
115 120 125

Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
130 135 140

Glu
145

<210> 85

<211> 145

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(145)

<223> Sequence of IBDV D6948-VP5

<400> 85

Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala
1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala

	20		25		30
Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His	35	40	45		
Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg	50	55	60		
Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly	65	70	75	80	
Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp	85	90	95		
Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala	100	105	110		
Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg	115	120	125		
Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro	130	135	140		
Glu					
145					

<210> 86
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBVD CEF94-VP5

<400> 86
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
1 5 10 15
Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
20 25 30
Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
35 40 45
Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
50 55 60
Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
65 70 75 80
Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
130 135 140

Glu
145

<210> 87

<211> 149

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(149)

<223> Sequence of IBDV D6948-VP5

<400> 87

Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp
1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu
20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro
35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys
50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp
65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln
85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln
100 105 110

Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr
115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu
130 135 140

Pro Arg Lys Pro Glu
145